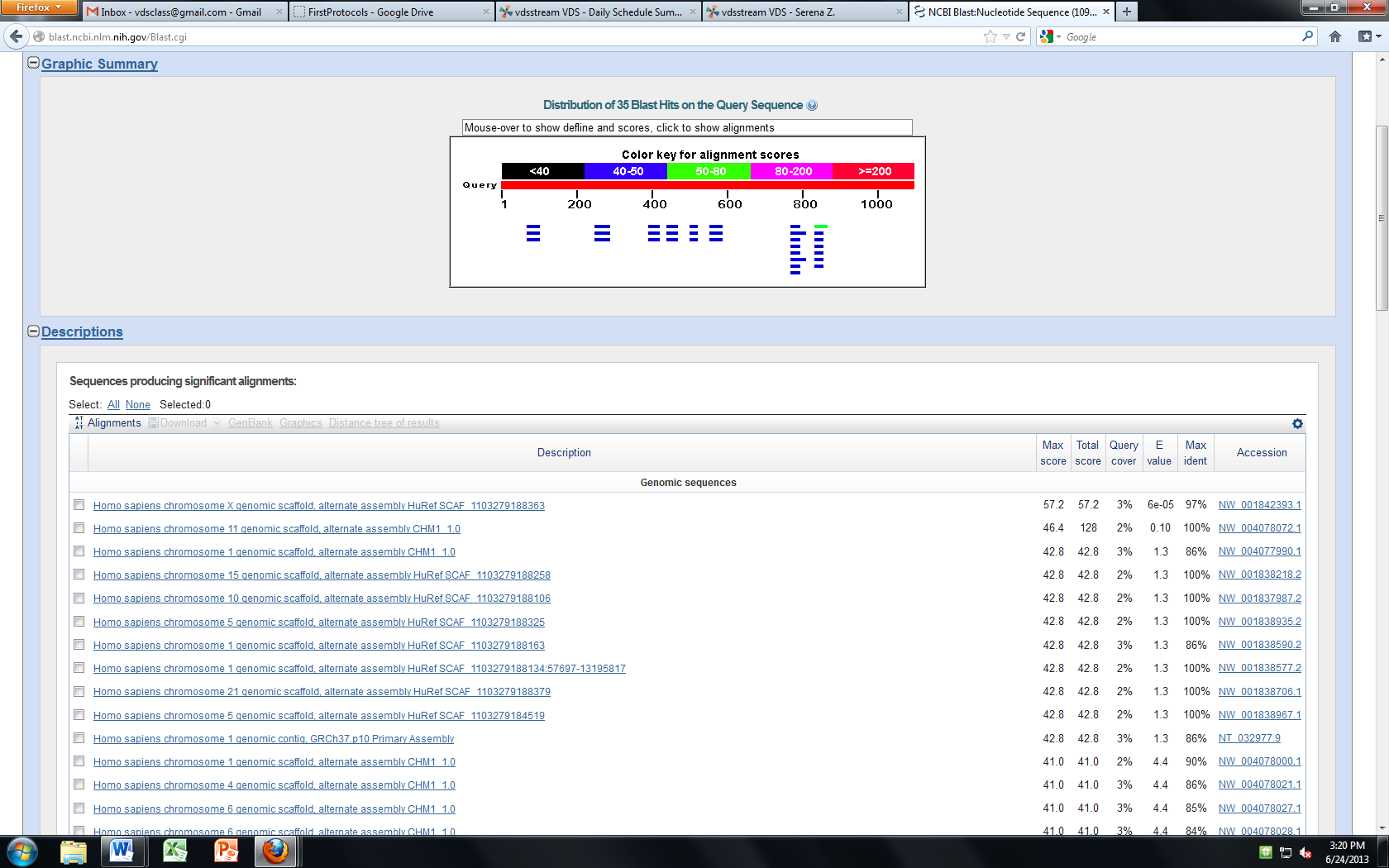
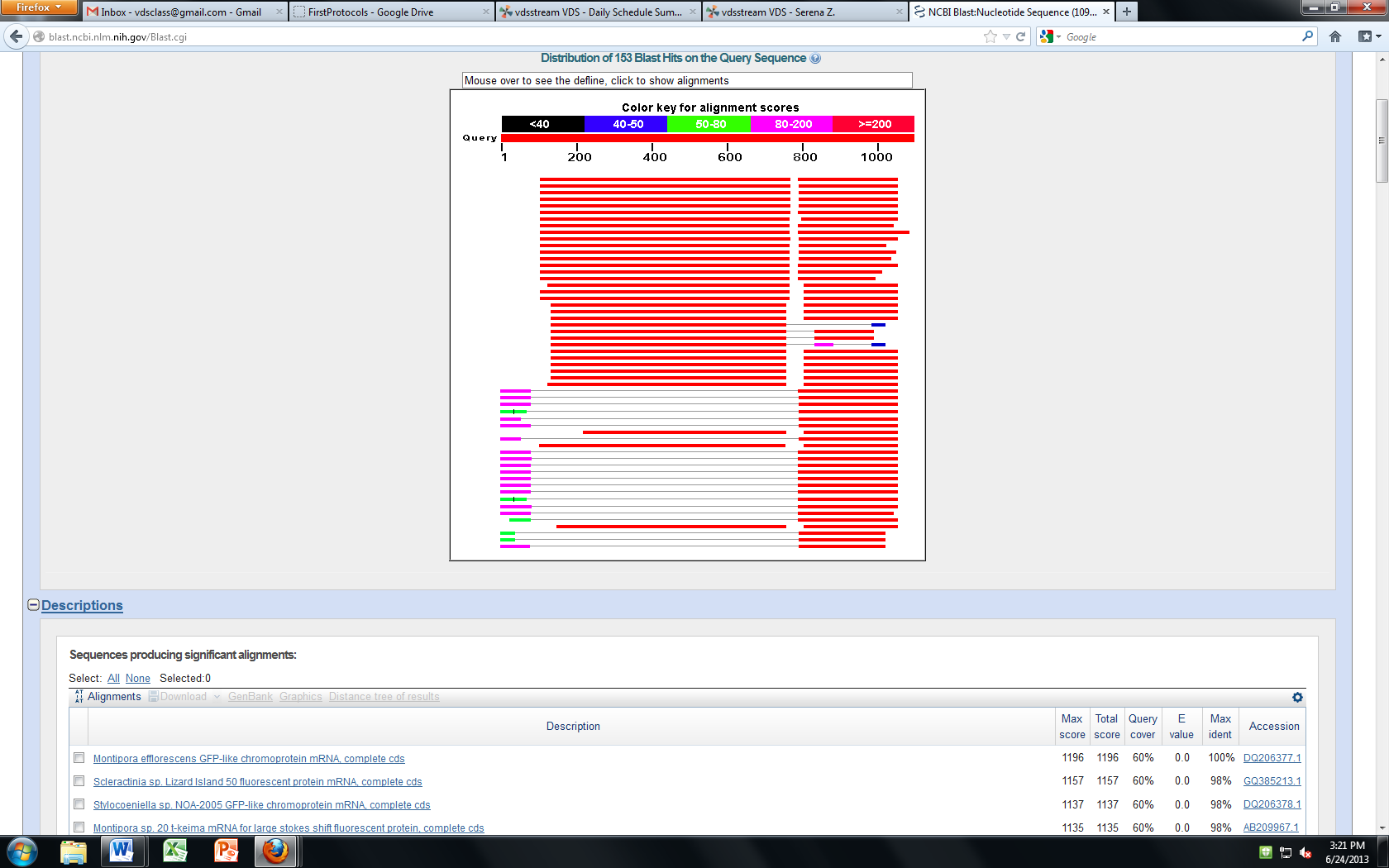
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CGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTTACCCAACTTAATCGCCTTGCAGCACATCCCCCTTTCGCCAGCTGGCGTAATAGCGAANAGGCCCGCACCGATCGCCCTTCCCACAGTTGCGCAGCCTGATGGCNATGGACGCNNCCTGNANCGNCGCATTAGCNCGGCNGGNNNGNGNNCNCGCAGCGNGACNCTACANTTNCNGCNNCNANCNNNNNCNTTCNNTTNTNCNNNTNNNNNNNNNNNNNNNTTNCCGNNAGNTNNAANNGGGGNNNNNNNNNATNNGNTNNNNNNNNNNCCAAANTGNNNGNNNNGNNNNNNNNGNNNNNNNNNNNNNNNNNNNNNNNGANCNNNNNNNNNNNNANNNNNNNNNNNCNNNNNAANNNNNCCNNTNNN

TATNGNATACTCAAGCTATGCATCCAACGCGTTGGGAGCTCTCCCATATGGTCGACCTGCAGGCGGCCGCACTAGTGATTTTGATTGATTGAAGGAGAAATATCATGAGTGTGATCGCTAAACAAATGACCTACAAGGTTTATATGTCAGGCACGGTCAATGGACACTACTTTGAGGTCGAAGGCGATGGAAAAGGAAAGCCTTACGAGGGGGAGCAGACGGTAAAGCTCACTGTCACCAAGGGTGGACCTCTGCCATTTGCTTGGGATATTTTATCACCACTGTCTCAATACGGAAGCATACCATTCACCAAGTACCCTGAAGACATCCCTGATTATGTAAAGCAGTCATTCCCTGAGGGATATACATGGGAGAGGATCATGAACTTTGAAGATGGTGCAGTGTGTACTGTCAGCAATGATTCCAGCATCCAAGGCAACTGTTTCATCTACAATGTCAAAATCTCTGGTGTGAACTTTCCTCCCAATGGACCTGTTATGCAGAAGAAGACACAGGGCTGGGAACCCAACACTGAGCGTCTCTTTGCACGAGATGGAATGCTGATAGGAAACAACTTTATGGCTCTGAAGTTGGAAGGAGGTGGTTACTATTTGTGTGAATTCAAATCTACTTACAAGGCAAAGAAGCCTGTGAGGATGCCAGGGTATCACTATGTTGACCGCAAACTGGATGTAACCAGTCACAACAAGGATTACACATTTGTTGAGCAGTGTGAAATATCCATTGCACGCCACTCTTTGCTCGGTCATCACCATCACCATCACTAAAATCCCGCGGCCATGGCGGCCGGGAGCATGCGACGTCGGGCCCAATTCGCCCTATAGTGAGTCGTATTACAATTCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTTACCCAACTTAATCGCCTTGCAGCACATCCCCCTTTCGCCAGCTGGCGTAATAGCGAANAGGCCCGCACCGATCGCCCTTCCCACAGTTGCGCAGCCTGATGGCNATGGACGCNNCCTGNANCGNCGCATTAGCNCGGCNGGNNNGNGNNCNCGCAGCGNGACNCTACANTTNCNGCNNCNANC





Sequence ID: lcl|7205Length: 1092Number of Matches: 1

Related Information

Range 1: 105 to 788[Graphics](http://www.ncbi.nlm.nih.gov/projects/sviewer/?RID=WHARMXM011N&id=lcl%7C7205&tracks=%5bkey:sequence_track,name:Sequence,display_name:Sequence,id:STD1,category:Sequence,annots:Sequence,ShowLabel:true%5d%5bkey:gene_model_track,CDSProductFeats:false%5d%5bkey:alignment_track,name:other%20alignments,annots:NG%20Alignments%7CRefseq%20Alignments%7CGnomon%20Alignments%7CUnnamed,shown:false%5d&v=71:822&appname=ncbiblast&link_loc=fromHSP) Next Match Previous Match

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Alignment statistics for match #1 | | | | |
| **Score** | **Expect** | **Identities** | **Gaps** | **Strand** |
| 1258 bits(681) | 0.0 | 683/684(99%) | 0/684(0%) | Plus/Plus |

Query 1 ATGAGTGTGATCGCTAAACAAATGACCTACAAGGTTTATATGTCAGGCACGGTCAATGGA 60

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 105 ATGAGTGTGATCGCTAAACAAATGACCTACAAGGTTTATATGTCAGGCACGGTCAATGGA 164

Query 61 CACTACTTTGAGGTCGAAGGCGATGGAAAAGGAAAGCCTTACGAGGGGGAGCAGACGGTA 120

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 165 CACTACTTTGAGGTCGAAGGCGATGGAAAAGGAAAGCCTTACGAGGGGGAGCAGACGGTA 224

Query 121 AAGCTCACTGTCACCAAGGGTGGACCTCTGCCATTTGCTTGGGATATTTTATCACCACTG 180

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 225 AAGCTCACTGTCACCAAGGGTGGACCTCTGCCATTTGCTTGGGATATTTTATCACCACTG 284

Query 181 TCTCAATACGGAAGCATACCATTCACCAAGTACCCTGAAGACATCCCTGATTATGTAAAG 240

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 285 TCTCAATACGGAAGCATACCATTCACCAAGTACCCTGAAGACATCCCTGATTATGTAAAG 344

Query 241 CAGTCATTCCCTGAGGGATATACATGGGAGAGGATCATGAACTTTGAAGATGGTGCAGTG 300

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 345 CAGTCATTCCCTGAGGGATATACATGGGAGAGGATCATGAACTTTGAAGATGGTGCAGTG 404

Query 301 TGTACTGTCAGCAATGATTCCAGCATCCAAGGCAACTGTTTCATCTACAATGTCAAAATC 360

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 405 TGTACTGTCAGCAATGATTCCAGCATCCAAGGCAACTGTTTCATCTACAATGTCAAAATC 464

Query 361 TCTGGTGTGAACTTTCCTCCCAATGGACCTGTTATGCAGAAGAAGACACAGGGCTGGGAA 420

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 465 TCTGGTGTGAACTTTCCTCCCAATGGACCTGTTATGCAGAAGAAGACACAGGGCTGGGAA 524

Query 421 CCCAACACTGAGCGTCTCTTTGCACGAGATGGAATGCTGATAGGAAACAACTTTATGGCT 480

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 525 CCCAACACTGAGCGTCTCTTTGCACGAGATGGAATGCTGATAGGAAACAACTTTATGGCT 584

Query 481 CTGAAGTTGGAAGGAGGTGGTTACTATTTGTGTGAGTTCAAATCTACTTACAAGGCAAAG 540

||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||

Sbjct 585 CTGAAGTTGGAAGGAGGTGGTTACTATTTGTGTGAATTCAAATCTACTTACAAGGCAAAG 644

Query 541 AAGCCTGTGAGGATGCCAGGGTATCACTATGTTGACCGCAAACTGGATGTAACCAGTCAC 600

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 645 AAGCCTGTGAGGATGCCAGGGTATCACTATGTTGACCGCAAACTGGATGTAACCAGTCAC 704

Query 601 AACAAGGATTACACATTTGTTGAGCAGTGTGAAATATCCATTGCACGCCACTCTTTGCTC 660

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 705 AACAAGGATTACACATTTGTTGAGCAGTGTGAAATATCCATTGCACGCCACTCTTTGCTC 764

Query 661 GGTCATCACCATCACCATCACTAA 684

||||||||||||||||||||||||

Sbjct 765 GGTCATCACCATCACCATCACTAA 788

Translate results

>rf 1 Untitled

YXILKLCIQRVGSSPIWSTCRRPH\*\*F\*LIEGEIS\*V\*SLNK\*PTRFICQARSMDTTLRS

KAMEKESLTRGSRR\*SSLSPRVDLCHLLGIFYHHCLNTEAYHSPSTLKTSLIM\*SSHSLR

DIHGRGS\*TLKMVQCVLSAMIPASKATVSSTMSKSLV\*TFLPMDLLCRRRHRAGNPTLSV

SLHEMEC\*\*ETTLWL\*SWKEVVTICVNSNLLTRQRSL\*GCQGITMLTANWM\*PVTTRITH

LLSSVKYPLHATLCSVITITITKIPRPWRPGACDVGPNSPYSESYYNSLAVVLQRRDWEN

PGVTQLNRLAAHPPFASWRNSEXARTDRPSHSCAA\*WXWTXPXXXH\*XGXXXXXQRDXTX

XAXX

>rf 2 Untitled

XXYSSYASNALGALPYGRPAGGRTSDFD\*LKEKYHECDR\*TNDLQGLYVRHGQWTLL\*GR

RRWKRKALRGGADGKAHCHQGWTSAICLGYFITTVSIRKHTIHQVP\*RHP\*LCKAVIP\*G

IYMGEDHEL\*RWCSVYCQQ\*FQHPRQLFHLQCQNLWCELSSQWTCYAEEDTGLGTQH\*AS

LCTRWNADRKQLYGSEVGRRWLLFV\*IQIYLQGKEACEDARVSLC\*PQTGCNQSQQGLHI

C\*AV\*NIHCTPLFARSSPSPSLKSRGHGGREHATSGPIRPIVSRITIHWPSFYNVVTGKT

LALPNLIALQHIPLSPAGVIAXRPAPIALPTVAQPDGXGRXLXRRISXAGXXXRSXTLXX

XXX

>rf 3 Untitled

XXTQAMHPTRWELSHMVDLQAAALVILID\*RRNIMSVIAKQMTYKVYMSGTVNGHYFEVE

GDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPLSQYGSIPFTKYPEDIPDYVKQSFPEG

YTWERIMNFEDGAVCTVSNDSSIQGNCFIYNVKISGVNFPPNGPVMQKKTQGWEPNTERL

FARDGMLIGNNFMALKLEGGGYYLCEFKSTYKAKKPVRMPGYHYVDRKLDVTSHNKDYTF

VEQCEISIARHSLLGHHHHHH\*NPAAMAAGSMRRRAQFAL\*\*VVLQFTGRRFTTS\*LGKP

WRYPT\*SPCSTSPFRQLA\*\*RXGPHRSPFPQLRSLMAMDAXXXXALARXXXXXAAXXYXX

XXX

RF3 seems to be the best reading frame because there is a methionine with a long, uninterrupted sequence of amino acids (before a stop codon is reached after the 6His tag). It is also the only RF that contains the 6His tag.

**ORF FINDER:**

LOCUS tmpseq\_0 1092 bp linear 24-JUN-2013

DEFINITION No definition line found.

ACCESSION tmpseq\_0

VERSION

KEYWORDS .

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

FEATURES Location/Qualifiers

source 1..1092

BASE COUNT 284 a 266 c 264 g 251 t 27 others

ORIGIN

1 tatngnatac tcaagctatg catccaacgc gttgggagct ctcccatatg gtcgacctgc

61 aggcggccgc actagtgatt ttgattgatt gaaggagaaa tatcatgagt gtgatcgcta

121 aacaaatgac ctacaaggtt tatatgtcag gcacggtcaa tggacactac tttgaggtcg

181 aaggcgatgg aaaaggaaag ccttacgagg gggagcagac ggtaaagctc actgtcacca

241 agggtggacc tctgccattt gcttgggata ttttatcacc actgtctcaa tacggaagca

301 taccattcac caagtaccct gaagacatcc ctgattatgt aaagcagtca ttccctgagg

361 gatatacatg ggagaggatc atgaactttg aagatggtgc agtgtgtact gtcagcaatg

421 attccagcat ccaaggcaac tgtttcatct acaatgtcaa aatctctggt gtgaactttc

481 ctcccaatgg acctgttatg cagaagaaga cacagggctg ggaacccaac actgagcgtc

541 tctttgcacg agatggaatg ctgataggaa acaactttat ggctctgaag ttggaaggag

601 gtggttacta tttgtgtgaa ttcaaatcta cttacaaggc aaagaagcct gtgaggatgc

661 cagggtatca ctatgttgac cgcaaactgg atgtaaccag tcacaacaag gattacacat

721 ttgttgagca gtgtgaaata tccattgcac gccactcttt gctcggtcat caccatcacc

781 atcactaaaa tcccgcggcc atggcggccg ggagcatgcg acgtcgggcc caattcgccc

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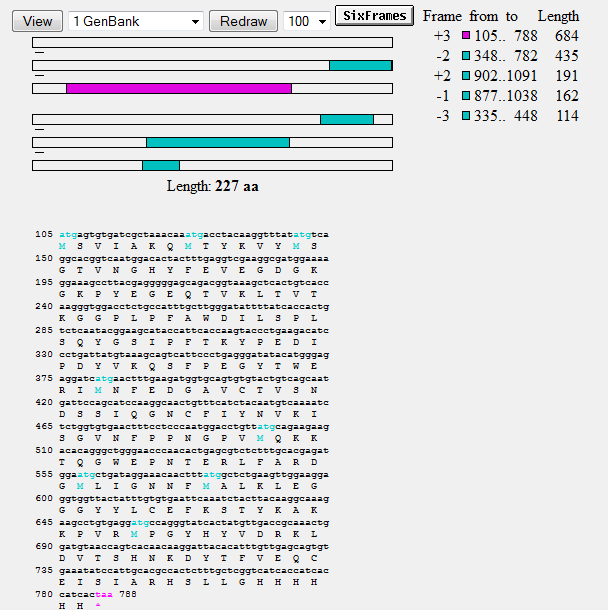
901 cctggcgtta cccaacttaa tcgccttgca gcacatcccc ctttcgccag ctggcgtaat

961 agcgaanagg cccgcaccga tcgcccttcc cacagttgcg cagcctgatg gcnatggacg

1021 cnncctgnan cgncgcatta gcncggcngg nnngngnncn cgcagcgnga cnctacantt

1081 ncngcnncna nc

//



PROTEIN TRANSLATION FOR PURPLE PROTEIN:

Translate results

>rf 1 Untitled

MSVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPL

SQYGSIPFTKYPEDIPDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCFIYNVKI

SGVNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGYYLCEFKSTYKAK

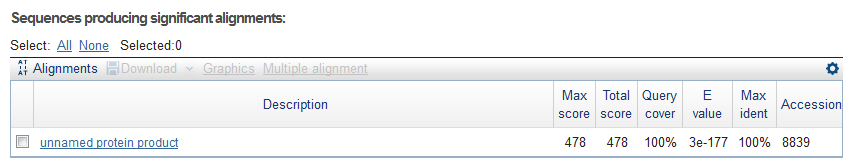
KPVRMPGYHYVDRKLDVTSHNKDYTFVEQCEISIARHSLLGHHHHHH\*

unnamed protein product

Sequence ID: lcl|8839Length: 228Number of Matches: 1

Related Information

Range 1: 1 to 227[Graphics](http://www.ncbi.nlm.nih.gov/projects/sviewer/?RID=WHCSATXK114&id=lcl%7C8839&tracks=%5bkey:sequence_track,name:Sequence,display_name:Sequence,id:STD1,category:Sequence,annots:Sequence,ShowLabel:true%5d%5bkey:gene_model_track,CDSProductFeats:false%5d%5bkey:alignment_track,name:other%20alignments,annots:NG%20Alignments%7CRefseq%20Alignments%7CGnomon%20Alignments%7CUnnamed,shown:false%5d&v=0:238&appname=ncbiblast&link_loc=fromHSP) Next Match Previous Match



|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Alignment statistics for match #1 | | | | | |
| **Score** | **Expect** | **Method** | **Identities** | **Positives** | **Gaps** |
| 478 bits(1229) | 3e-177 | Compositional matrix adjust. | 227/227(100%) | 227/227(100%) | 0/227(0%) |

Query 1 MSVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPL 60

MSVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPL

Sbjct 1 MSVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPL 60

Query 61 SQYGSIPFTKYPEDIPDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCFIYNVKI 120

SQYGSIPFTKYPEDIPDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCFIYNVKI

Sbjct 61 SQYGSIPFTKYPEDIPDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCFIYNVKI 120

Query 121 SGVNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGYYLCEFKSTYKAK 180

SGVNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGYYLCEFKSTYKAK

Sbjct 121 SGVNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGYYLCEFKSTYKAK 180

Query 181 KPVRMPGYHYVDRKLDVTSHNKDYTFVEQCEISIARHSLLGHHHHHH 227

KPVRMPGYHYVDRKLDVTSHNKDYTFVEQCEISIARHSLLGHHHHHH

Sbjct 181 KPVRMPGYHYVDRKLDVTSHNKDYTFVEQCEISIARHSLLGHHHHHH 227

**Pgemt sequence:**

1. GGGCGAATTG GGCCCGACGT CGCATGCTCC CGGCCGCCAT GGCCGCGGGA  
     
     51  TTAATCACTAGT GCGGCCGCCT GCAGGTCGAC CATATGGGAG AGCTCCCAAC  
     
   101  GCGTTGGATG CATAGCTTGA GTATTCTATA GTGTCACCTA AATAGCTTGG  
     
   151  CGTAATCATG GTCATAGCTG TTTCCTGTGT GAAATTGTTA TCCGCTCACA  
     
   201  ATTCCACACA ACATACGAGC CGGAAGCATA AAGTGTAAAG CCTGGGGTGC  
     
   251  CTAATGAGTG AGCTAACTCA CATTAATTGC GTTGCGCTCA CTGCCCGCTT  
     
   301  TCCAGTCGGG AAACCTGTCG TGCCAGCTGC ATTAATGAAT CGGCCAACGC  
     
   351  GCGGGGAGAG GCGGTTTGCG TATTGGGCGC TCTTCCGCTT CCTCGCTCAC  
     
   401  TGACTCGCTG CGCTCGGTCG TTCGGCTGCG GCGAGCGGTA TCAGCTCACT  
     
   451  CAAAGGCGGT AATACGGTTA TCCACAGAAT CAGGGGATAA CGCAGGAAAG  
     
   501  AACATGTGAG CAAAAGGCCA GCAAAAGGCC AGGAACCGTA AAAAGGCCGC  
     
   551  GTTGCTGGCG TTTTTCCATA GGCTCCGCCC CCCTGACGAG CATCACAAAA  
     
   601  ATCGACGCTC AAGTCAGAGG TGGCGAAACC CGACAGGACT ATAAAGATAC  
     
   651  CAGGCGTTTC CCCCTGGAAG CTCCCTCGTG CGCTCTCCTG TTCCGACCCT  
     
   701  GCCGCTTACC GGATACCTGT CCGCCTTTCT CCCTTCGGGA AGCGTGGCGC  
     
   751  TTTCTCATAG CTCACGCTGT AGGTATCTCA GTTCGGTGTA GGTCGTTCGC  
     
   801  TCCAAGCTGG GCTGTGTGCA CGAACCCCCC GTTCAGCCCG ACCGCTGCGC  
     
   851  CTTATCCGGT AACTATCGTC TTGAGTCCAA CCCGGTAAGA CACGACTTAT  
     
   901  CGCCACTGGC AGCAGCCACT GGTAACAGGA TTAGCAGAGC GAGGTATGTA  
     
   951  GGCGGTGCTA CAGAGTTCTT GAAGTGGTGG CCTAACTACG GCTACACTAG  
     
   1001 AAGAACAGTA TTTGGTATCT GCGCTCTGCT GAAGCCAGTT ACCTTCGGAA  
     
   1051 AAAGAGTTGG TAGCTCTTGA TCCGGCAAAC AAACCACCGC TGGTAGCGGT  
     
   1101 GGTTTTTTTG TTTGCAAGCA GCAGATTACG CGCAGAAAAA AAGGATCTCA  
     
   1151 AGAAGATCCT TTGATCTTTT CTACGGGGTC TGACGCTCAG TGGAACGAAA  
     
   1201 ACTCACGTTA AGGGATTTTG GTCATGAGAT TATCAAAAAG GATCTTCACC  
     
   1251 TAGATCCTTT TAAATTAAAA ATGAAGTTTT AAATCAATCT AAAGTATATA  
     
   1301 TGAGTAAACT TGGTCTGACA GTTACCAATG CTTAATCAGT GAGGCACCTA  
     
   1351 TCTCAGCGAT CTGTCTATTT CGTTCATCCA TAGTTGCCTG ACTCCCCGTC  
     
   1401 GTGTAGATAA CTACGATACG GGAGGGCTTA CCATCTGGCC CCAGTGCTGC  
     
   1451 AATGATACCG CGAGACCCAC GCTCACCGGC TCCAGATTTA TCAGCAATAA  
     
   1501 ACCAGCCAGC CGGAAGGGCC GAGCGCAGAA GTGGTCCTGC AACTTTATCC  
     
   1551 GCCTCCATCC AGTCTATTAA TTGTTGCCGG GAAGCTAGAG TAAGTAGTTC  
     
   1601 GCCAGTTAAT AGTTTGCGCA ACGTTGTTGC CATTGCTACA GGCATCGTGG  
     
   1651 TGTCACGCTC GTCGTTTGGT ATGGCTTCAT TCAGCTCCGG TTCCCAACGA  
     
   1701 TCAAGGCGAG TTACATGATC CCCCATGTTG TGCAAAAAAG CGGTTAGCTC  
     
   1751 CTTCGGTCCT CCGATCGTTG TCAGAAGTAA GTTGGCCGCA GTGTTATCAC  
     
   1801 TCATGGTTAT GGCAGCACTG CATAATTCTC TTACTGTCAT GCCATCCGTA  
     
   1851 AGATGCTTTT CTGTGACTGG TGAGTACTCA ACCAAGTCAT TCTGAGAATA  
     
   1901 GTGTATGCGG CGACCGAGTT GCTCTTGCCC GGCGTCAATA CGGGATAATA  
     
   1951 CCGCGCCACA TAGCAGAACT TTAAAAGTGC TCATCATTGG AAAACGTTCT  
     
   2001 TCGGGGCGAA AACTCTCAAG GATCTTACCG CTGTTGAGAT CCAGTTCGAT  
     
   2051 GTAACCCACT CGTGCACCCA ACTGATCTTC AGCATCTTTT ACTTTCACCA  
     
   2101 GCGTTTCTGG GTGAGCAAAA ACAGGAAGGC AAAATGCCGC AAAAAAGGGA  
     
   2151 ATAAGGGCGA CACGGAAATG TTGAATACTC ATACTCTTCC TTTTTCAATA  
     
   2201 TTATTGAAGC ATTTATCAGG GTTATTGTCT CATGAGCGGA TACATATTTG  
     
   2251 AATGTATTTA GAAAAATAAA CAAATAGGGG TTCCGCGCAC ATTTCCCCGA  
     
   2301 AAAGTGCCAC CTGATGCGGT GTGAAATACC GCACAGATGC GTAAGGAGAA  
     
   2351 AATACCGCAT CAGGAAATTG TAAGCGTTAA TATTTTGTTA AAATTCGCGT  
     
   2401 TAAATTTTTG TTAAATCAGC TCATTTTTTA ACCAATAGGC CGAAATCGGC  
     
   2451 AAAATCCCTT ATAAATCAAA AGAATAGACC GAGATAGGGT TGAGTGTTGT  
     
   2501 TCCAGTTTGG AACAAGAGTC CACTATTAAA GAACGTGGAC TCCAACGTCA  
     
   2551 AAGGGCGAAA AACCGTCTAT CAGGGCGATG GCCCACTACG TGAACCATCA  
     
   2601 CCCTAATCAA GTTTTTTGGG GTCGAGGTGC CGTAAAGCAC TAAATCGGAA  
     
   2651 CCCTAAAGGG AGCCCCCGAT TTAGAGCTTG ACGGGGAAAG CCGGCGAACG  
     
   2701 TGGCGAGAAA GGAAGGGAAG AAAGCGAAAG GAGCGGGCGC TAGGGCGCTG  
     
   2751 GCAAGTGTAG CGGTCACGCT GCGCGTAACC ACCACACCCG CCGCGCTTAA  
     
   2801 TGCGCCGCTA CAGGGCGCGT CCATTCGCCA TTCAGGCTGC GCAACTGTTG  
     
   2851 GGAAGGGCGA TCGGTGCGGG CCTCTTCGCT ATTACGCCAG CTGGCGAAAG  
     
   2901 GGGGATGTGC TGCAAGGCGA TTAAGTTGGG TAACGCCAGG GTTTTCCCAG  
     
   2951 TCACGACGTT GTAAAACGAC GGCCAGTGAA TTGTAATACG ACTCACTATA

Reverse complement:

TATAGTGAGTCGTATTACAATTCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAAC

CCTGGCGTTACCCAACTTAATCGCCTTGCAGCACATCCCCCTTTCGCCAGCTGGCGTAAT

AGCGAAGAGGCCCGCACCGATCGCCCTTCCCAACAGTTGCGCAGCCTGAATGGCGAATGG

ACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGACCG

CTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCGCCA

CGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGATTTA

GTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTGGGC

CATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATAGTG

GACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATTTAT

AAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAATTTA

ACGCGAATTTTAACAAAATATTAACGCTTACAATTTCCTGATGCGGTATTTTCTCCTTAC

GCATCTGTGCGGTATTTCACACCGCATCAGGTGGCACTTTTCGGGGAAATGTGCGCGGAA

CCCCTATTTGTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATAAC

CCTGATAAATGCTTCAATAATATTGAAAAAGGAAGAGTATGAGTATTCAACATTTCCGTG

TCGCCCTTATTCCCTTTTTTGCGGCATTTTGCCTTCCTGTTTTTGCTCACCCAGAAACGC

TGGTGAAAGTAAAAGATGCTGAAGATCAGTTGGGTGCACGAGTGGGTTACATCGAACTGG

ATCTCAACAGCGGTAAGATCCTTGAGAGTTTTCGCCCCGAAGAACGTTTTCCAATGATGA

GCACTTTTAAAGTTCTGCTATGTGGCGCGGTATTATCCCGTATTGACGCCGGGCAAGAGC

AACTCGGTCGCCGCATACACTATTCTCAGAATGACTTGGTTGAGTACTCACCAGTCACAG

AAAAGCATCTTACGGATGGCATGACAGTAAGAGAATTATGCAGTGCTGCCATAACCATGA

GTGATAACACTGCGGCCAACTTACTTCTGACAACGATCGGAGGACCGAAGGAGCTAACCG

CTTTTTTGCACAACATGGGGGATCATGTAACTCGCCTTGATCGTTGGGAACCGGAGCTGA

ATGAAGCCATACCAAACGACGAGCGTGACACCACGATGCCTGTAGCAATGGCAACAACGT

TGCGCAAACTATTAACTGGCGAACTACTTACTCTAGCTTCCCGGCAACAATTAATAGACT

GGATGGAGGCGGATAAAGTTGCAGGACCACTTCTGCGCTCGGCCCTTCCGGCTGGCTGGT

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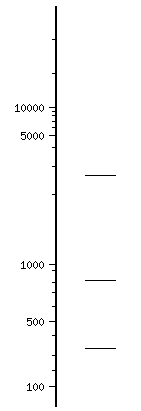
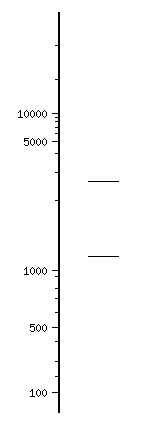
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1 kb ladder + EcoRI PvuII EcoRI+PvuII

